

**Modern Achievements in Population, Evolutionary, and Ecological Genetics :
International Symposium, Vladivostok – Vostok Marine Biological Station,
September 6–12, 2009 : Program & Abstracts. – Vladivostok, 2009. –53 p. – Engl.
ISBN 978-5-7442-1483-8**

HELD BY:

*Vladivostok Public Foundation for Development of Genetics,
Far Eastern Branch of Russian Academy of Sciences,
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SPONSORS:

*Far Eastern Branch of Russian Academy of Sciences,
Russian Foundation for Basic Research
Nakhodka City Territorial Ecological Foundation
Moscow Rep Office of Corporation "Applera International Inc." (USA)*

Editor Yuri Ph. Kartavtsev

**Современные достижения в популяционной, эволюционной и
экологической генетике : Международный симпозиум, Владивосток –
Морская биологическая станция “Восток”, 6–12 сентября 2009 : Программа и
тезисы докладов. – Владивосток, 2009. –53 с. – Англ.**

ОРГАНИЗАТОРЫ:

*Владивостокский общественный фонд развития генетики,
Дальневосточное отделение РАН,
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ФИНАНСОВАЯ ПОДДЕРЖКА:

*Дальневосточное отделение РАН,
Российский фонд фундаментальных исследований
Территориальный экологический фонд г. Находка*

Ответственный редактор Ю.Ф. Картавец

ISBN 978-5-7442-1483-8

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**POPULATION-GENETIC STRUCTURE OF RARE PLANT ARISTOLOCHIA
CONTORTA BUNGE (ARISTOLOCHIACEAE)**

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Aristolochia contorta Bunge is a unique herbaceous liana of the Russian Far East, where this plant is represented by a few small fragmented and badly exhausted populations in the southwest part of the Primorskij Krai and in the Jewish Autonomous Region only. Besides that, the species area covers Japan, Korea and some province of China; however, any information about the state of *A. contorta* on these territories is limited. In Russia, the species is listed in the Red Data Book of the Primorsky Krai as a vulnerable species. This plant is rare in nature presumably through its sensitivity to destructive changes of habitats. Loss of reproductive individuals was observed for the last years substantially due to intensified anthropogenic influence as well. In addition, *A. contorta* is a valuable medicine plant and its collection for an herbal remedy contributes to reduction of its natural populations. Now these populations need in protection and restoring. It would be a specially important for the conserving not only this species, but also for the closely connected with *A. contorta* a relict butterfly, *Sericinus montela* Gray, for which this plant is the single feed source.

Yet, the species genetic variability has not studied by now. In this work we try to estimate genetic variation and differentiation of the Russian populations of *A. contorta* using allozyme markers.

Samples were collected in 4 natural *A. contorta* populations located along Petrovka, Suiphun and Razdol'naya rivers. Electrophoretic analysis of nine *A. contorta* enzymes revealed 32 different electrophoretic variants, presumably encoded by 23 loci. Five loci (*Aat-1*, *Fe-1*, *Fe-2*, *6-Pgd-2*, *Lap*) were polymorphic.

The results show that polymorphism of the *A. contorta* populations is lower than in average for plants. Averaged over the populations, the proportion of polymorphic loci (P) was 21.74%; the number of alleles per locus (A) was 1.39. The observed heterozygosity was equal to the expected heterozygosity, being on average 9%. The highest level of the genetic variation was revealed in the population of the Oktiabr'skii region, whereas the lowest one was found in the Bol'shoi Kamen' population. This fact may be explained by the most anthropogenic pressure on this territory. Allozyme analysis has shown some difference in allele set of *Lap* locus between all localities studied. Differences in allele frequencies among populations were statistically significant over all loci. The Wright's F -statistics analysis revealed small excess of heterozygotes in the populations and, simultaneously, about 16% heterozygote deficiency for the whole species. These data may be an evidence of subdivision of the species into separate small reproductive groups. The differentiation index F_{ST} varied from 0.070 to 0.252 for different loci, being on average 0.16 for all loci. This value is high enough and means that about 16.2% of the total variation is accounted for the inter-population variation component. It is known, that population differentiation is connected to gene flow. This parameter was 1.29 among all populations. Obviously, gene flow between populations studied is not high enough for preventing of destructive consequences of genetic drift within small localities.

Thus, the research showed a low level of genetic diversity and high level of genetic differentiation between Russian *A. contorta* populations. The data supposed that all the populations of *A. contorta* in Primorskij Krai have common gene pool. Today the genetic drift is contributing the main input to the population genetic structure of the *A. contorta*. The genetic drift connected with the reduction of population reproductive and effective sizes, which might be increased in part by the anthropogenic impact.